SEQUENCE LISTING

<110> Friddle, Carl Johan
       Hilbun, Erin

<120> Novel Human Proteases and Polynucleotides Encoding the Same

<130> LEX-0241-USA

<150> US 60/236,689
<151> 2000-09-29

<160> 7

<170> FastSEQ for Windows Version 4.0

<210> 1
<211> 966
<212> DNA
<213> homo sapiens

<400> 1
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caggaggact tttacctaca cctgacgccg gatgctcagt tcttggctcc cgccttctcc     240
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tgcttctatt ctggggacgt gaacgccgag ccggactcgt tcgctgctgt gagcctgtgc     360
ggggggctcc gcggagcctt tggctaccga ggcgccgagt atgtcattag cccgctgccc     420
aatgctagcg cgccggcggc gcagcgcaac agccagggcg cacaccttct ccagcgccgg     480
ggtgttccgg gcgggccttc cggagacccc acctctcgct gcggggtggc ctcgggctgg     540
aaccccgcca tcctacgggc cctggaccct tacaagccgc ggcgggcggg cttcggggag     600
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gagacgctgg tggtcgcgga cgagtcaatg gtcaagttcc acggcgcgga cctggaacat     720
tatctgctga cgctgctggc aacggcggcg cgactctacc gccatcccag catcctcaac     780
cccatcaaca tcgttgtggt caaggtgctg cttcttagag atcgtgactc cgggcccaag     840
gtcaccggca atgcggccct gacgctgcgc aacttctgtg cctggcagaa gaagctgaac     900
aaagtgagtg acaagcaccc cgagtactgg gacactgcca tcctcttcac caggcaggag     960
agttga                                                                 966
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<210> 2
<211> 321
<212> PRT
<213> homo sapiens

<400> 2
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Met Leu Leu Leu Gly Ile Leu Thr Leu Ala Phe Ala Gly Arg Thr Ala
1               5                   10                  15
Gly Gly Ser Glu Pro Glu Arg Glu Val Val Val Pro Ile Arg Leu Asp
            20                  25                  30
Pro Asp Ile Asn Gly Arg Arg Tyr Tyr Trp Arg Gly Pro Glu Asp Ser
            35                  40                  45
Gly Asp Gln Gly Leu Ile Phe Gln Ile Thr Ala Phe Gln Glu Asp Phe
        50                  55                  60
Tyr Leu His Leu Thr Pro Asp Ala Gln Phe Leu Ala Pro Ala Phe Ser
```

1

```
        65                      70                      75                      80
Thr Glu His Leu Gly Val Pro Leu Gln Gly Leu Thr Gly Gly Ser Ser
                        85                      90                      95
Asp Leu Arg Arg Cys Phe Tyr Ser Gly Asp Val Asn Ala Glu Pro Asp
            100                     105                     110
Ser Phe Ala Ala Val Ser Leu Cys Gly Gly Leu Arg Gly Ala Phe Gly
            115                     120                     125
Tyr Arg Gly Ala Glu Tyr Val Ile Ser Pro Leu Pro Asn Ala Ser Ala
        130                     135                     140
Pro Ala Ala Gln Arg Asn Ser Gln Gly Ala His Leu Leu Gln Arg Arg
145                     150                     155                     160
Gly Val Pro Gly Gly Pro Ser Gly Asp Pro Thr Ser Arg Cys Gly Val
                165                     170                     175
Ala Ser Gly Trp Asn Pro Ala Ile Leu Arg Ala Leu Asp Pro Tyr Lys
            180                     185                     190
Pro Arg Arg Ala Gly Phe Gly Glu Ser Arg Ser Arg Arg Arg Ser Gly
            195                     200                     205
Arg Ala Lys Arg Phe Val Ser Ile Pro Arg Tyr Val Glu Thr Leu Val
        210                     215                     220
Val Ala Asp Glu Ser Met Val Lys Phe His Gly Ala Asp Leu Glu His
225                     230                     235                     240
Tyr Leu Leu Thr Leu Leu Ala Thr Ala Ala Arg Leu Tyr Arg His Pro
                245                     250                     255
Ser Ile Leu Asn Pro Ile Asn Ile Val Val Val Lys Val Leu Leu Leu
                260                     265                     270
Arg Asp Arg Asp Ser Gly Pro Lys Val Thr Gly Asn Ala Ala Leu Thr
                275                     280                     285
Leu Arg Asn Phe Cys Ala Trp Gln Lys Lys Leu Asn Lys Val Ser Asp
        290                     295                     300
Lys His Pro Glu Tyr Trp Asp Thr Ala Ile Leu Phe Thr Arg Gln Glu
305                     310                     315                     320
Ser
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<210> 3
<211> 2853
<212> DNA
<213> homo sapiens

<400> 3

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tactggcggg gtcccgagga ctccgggggat cagggactca tttttcagat cacagcattt    180
caggaggact tttacctaca cctgacgccg gatgctcagt tcttggctcc cgccttctcc     240
actgagcatc tgggcgtccc cctccagggg ctcaccgggg gctcttcaga cctgcgacgc     300
tgcttctatt ctggggacgt gaacgccgag ccggactcgt cgctgctgt gagcctgtgc      360
ggggggctcc gcggagcctt ggctaccga ggcgccgagt atgtcattag cccgctgccc      420
aatgctagcg cgccggcggc gcagcgcaac agccagggcg cacaccttct ccagcgccgg     480
ggtgttccgg gcgggccttc cggagacccc acctctcgct gcggggtggc ctcgggctgg    540
aaccccgcca tcctacgggc cctggaccct tacaagccgc ggcgggcggg cttcggggag     600
agtcgtagcc ggcgcaggtc tgggcgcgcc aagcgtttcg tgtctatccc gcggtacgtg     660
gagacgctgg tggtcgcgga cgagtcaatg gtcaagttcc acggcgcgga cctggaacat    720
tatctgctga cgctgctggc aacggcggcg cgactctacc gccatcccag catcctcaac    780
cccatcaaca tcgttgtggt caaggtgctg cttcttagag atcgtgactc cgggcccaag     840
gtcaccggca atgcggccct gacgctgcgc aacttctgtg cctggcagaa gaagctgaac    900
aaagtgagtg acaagcaccc cgagtactgg gacactgcca tcctcttcac caggcaggac    960
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2

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ctgtgtggag ccaccacctg tgacaccctg ggcatggctg atgtgggtac catgtgtgac    1020
cccaagagaa gctgctctgt cattgaggac gatgggcttc catcagcctt caccactgcc    1080
cacgagctgg gccacgtgtt caacatgccc catgacaatg tgaaagtctg tgaggaggtg    1140
tttgggaagc tccgagccaa ccacatgatg tccccgaccc tcatccagat cgaccgtgcc    1200
aacccctggt cagcctgcag tgctgccatc atcaccgact tcctggacag cgggcacggt    1260
gactgcctcc tggaccaacc cagcaagccc atctccctgc ccgaggatct gccgggcgcc    1320
agctacaccc tgagccagca gtgcgagctg gcttttggcg tgggctccaa gccctgtcct    1380
tacatgcagt actgcaccaa gctgtggtgc accgggaagg ccaagggaca gatggtgtgc    1440
cagacccgcc acttcccctg ggccgatggc accagctgtg gcgagggcaa gctctgcctc    1500
aaaggggcct gcgtggagag acacaacctc aacaagcaca gggtggatgg ttcctgggcc    1560
aaatgggatc cctatggccc ctgctcgcgc acatgtggtg ggggcgtgca gctggccagg    1620
aggcagtgca ccaaccccac ccctgccaac ggggggcaagt actgcgaggg agtgagggtg    1680
aaataccgat cctgcaatct ggagccctgc cccagctcag cctccggaaa gagcttccgg    1740
gaggagcagt gtgaggcttt caacggctac aaccacagca ccaaccggct cactctcgcc    1800
gtggcatggg tgcccaagta ctccggcgtg tctccccggg acaagtgcaa gctcatctgc    1860
cgagccaatg gcactggcta cttctatgtg ctggcaccca aggtggtgga cggcacgctg    1920
tgctctcctg actccacctc cgtctgtgtc caaggcaagt gcatcaaggc tggctgtgat    1980
gggaacctgg gctccaagaa gagattcgac aagtgtgggg tgtgtggggg agacaataag    2040
agctgcaaga aggtgactgg actcttcacc aagcccatgc atggctacaa tttcgtggtg    2100
gccatccccg caggcgcctc aagcatcgac atccgccagc gcggttacaa agggctgatc    2160
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ttcgtggtgt cggcggtgga gcgggacctg gtggtgaagg gcagtctgct gcggtacagc    2280
ggcacgggca cagcggtgga gagcctgcag gcttcccggc ccatcctgga gccgctgacc    2340
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cccaaagagc tcgggagga caagtcctct catcccaagg acccccgggg aaccctctgtc    2460
ttgcacaaca gcgtcctcag cctctccaac caggtggagc agccggacga caggcccccct    2520
gcacgctggg tggctggcag ctggggggcg tgctccgcga gctgcggcag tggcctgcag    2580
aagcgggcgg tggactgtcg gggctccgcc gggcagcgca cggtccctgc ctgtgatgca    2640
gcccatcggc ccgtggagac acaagcctgc ggggagccct gccccacctg ggagctcagc    2700
gcctggtcac cctgctccaa gagctgcggc cggggatttc agaggcgctc actcaagtgt    2760
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<210> 4
<211> 950
<212> PRT
<213> homo sapiens

<400> 4
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Gly Gly Ser Glu Pro Glu Arg Glu Val Val Val Pro Ile Arg Leu Asp
            20                  25                  30
Pro Asp Ile Asn Gly Arg Arg Tyr Tyr Trp Arg Gly Pro Glu Asp Ser
            35                  40                  45
Gly Asp Gln Gly Leu Ile Phe Gln Ile Thr Ala Phe Gln Glu Asp Phe
        50                  55                  60
Tyr Leu His Leu Thr Pro Asp Ala Gln Phe Leu Ala Pro Ala Phe Ser
65                  70                  75                  80
Thr Glu His Leu Gly Val Pro Leu Gln Gly Leu Thr Gly Gly Ser Ser
                85                  90                  95
Asp Leu Arg Arg Cys Phe Tyr Ser Gly Asp Val Asn Ala Glu Pro Asp
            100                 105                 110
Ser Phe Ala Ala Val Ser Leu Cys Gly Gly Leu Arg Gly Ala Phe Gly
        115                 120                 125
Tyr Arg Gly Ala Glu Tyr Val Ile Ser Pro Leu Pro Asn Ala Ser Ala
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3

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Pro Ala Ala Gln Arg Asn Ser Gln Gly Ala His Leu Leu Gln Arg Arg
145                     150                     155                     160
Gly Val Pro Gly Gly Pro Ser Gly Asp Pro Thr Ser Arg Cys Gly Val
                    165                     170                     175
Ala Ser Gly Trp Asn Pro Ala Ile Leu Arg Ala Leu Asp Pro Tyr Lys
                    180                     185                     190
Pro Arg Arg Ala Gly Phe Gly Glu Ser Arg Ser Arg Arg Arg Ser Gly
                    195                     200                     205
Arg Ala Lys Arg Phe Val Ser Ile Pro Arg Tyr Val Glu Thr Leu Val
          210                     215                     220
Val Ala Asp Glu Ser Met Val Lys Phe His Gly Ala Asp Leu Glu His
225                     230                     235                     240
Tyr Leu Leu Thr Leu Leu Ala Thr Ala Ala Arg Leu Tyr Arg His Pro
                    245                     250                     255
Ser Ile Leu Asn Pro Ile Asn Ile Val Val Val Lys Val Leu Leu Leu
                    260                     265                     270
Arg Asp Arg Asp Ser Gly Pro Lys Val Thr Gly Asn Ala Ala Leu Thr
                    275                     280                     285
Leu Arg Asn Phe Cys Ala Trp Gln Lys Lys Leu Asn Lys Val Ser Asp
          290                     295                     300
Lys His Pro Glu Tyr Trp Asp Thr Ala Ile Leu Phe Thr Arg Gln Asp
305                     310                     315                     320
Leu Cys Gly Ala Thr Thr Cys Asp Thr Leu Gly Met Ala Asp Val Gly
                    325                     330                     335
Thr Met Cys Asp Pro Lys Arg Ser Cys Ser Val Ile Glu Asp Asp Gly
                    340                     345                     350
Leu Pro Ser Ala Phe Thr Thr Ala His Glu Leu Gly His Val Phe Asn
                    355                     360                     365
Met Pro His Asp Asn Val Lys Val Cys Glu Glu Val Phe Gly Lys Leu
          370                     375                     380
Arg Ala Asn His Met Met Ser Pro Thr Leu Ile Gln Ile Asp Arg Ala
385                     390                     395                     400
Asn Pro Trp Ser Ala Cys Ser Ala Ala Ile Ile Thr Asp Phe Leu Asp
                    405                     410                     415
Ser Gly His Gly Asp Cys Leu Leu Asp Gln Pro Ser Lys Pro Ile Ser
                    420                     425                     430
Leu Pro Glu Asp Leu Pro Gly Ala Ser Tyr Thr Leu Ser Gln Gln Cys
          435                     440                     445
Glu Leu Ala Phe Gly Val Gly Ser Lys Pro Cys Pro Tyr Met Gln Tyr
          450                     455                     460
Cys Thr Lys Leu Trp Cys Thr Gly Lys Ala Lys Gly Gln Met Val Cys
465                     470                     475                     480
Gln Thr Arg His Phe Pro Trp Ala Asp Gly Thr Ser Cys Gly Glu Gly
                    485                     490                     495
Lys Leu Cys Leu Lys Gly Ala Cys Val Glu Arg His Asn Leu Asn Lys
                    500                     505                     510
His Arg Val Asp Gly Ser Trp Ala Lys Trp Asp Pro Tyr Gly Pro Cys
          515                     520                     525
Ser Arg Thr Cys Gly Gly Gly Val Gln Leu Ala Arg Arg Gln Cys Thr
          530                     535                     540
Asn Pro Thr Pro Ala Asn Gly Gly Lys Tyr Cys Glu Gly Val Arg Val
545                     550                     555                     560
Lys Tyr Arg Ser Cys Asn Leu Glu Pro Cys Pro Ser Ser Ala Ser Gly
                    565                     570                     575
Lys Ser Phe Arg Glu Glu Gln Cys Glu Ala Phe Asn Gly Tyr Asn His
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4

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                 580                        585                        590
     Ser Thr Asn Arg Leu Thr Leu Ala Val Ala Trp Val Pro Lys Tyr Ser
             595                        600                        605
     Gly Val Ser Pro Arg Asp Lys Cys Lys Leu Ile Cys Arg Ala Asn Gly
         610                        615                        620
     Thr Gly Tyr Phe Tyr Val Leu Ala Pro Lys Val Val Asp Gly Thr Leu
     625                        630                        635                        640
     Cys Ser Pro Asp Ser Thr Ser Val Cys Val Gln Gly Lys Cys Ile Lys
                     645                        650                        655
     Ala Gly Cys Asp Gly Asn Leu Gly Ser Lys Lys Arg Phe Asp Lys Cys
                 660                        665                        670
     Gly Val Cys Gly Gly Asp Asn Lys Ser Cys Lys Lys Val Thr Gly Leu
             675                        680                        685
     Phe Thr Lys Pro Met His Gly Tyr Asn Phe Val Val Ala Ile Pro Ala
         690                        695                        700
     Gly Ala Ser Ser Ile Asp Ile Arg Gln Arg Gly Tyr Lys Gly Leu Ile
     705                        710                        715                        720
     Gly Asp Asp Asn Tyr Leu Ala Leu Lys Asn Ser Gln Gly Lys Tyr Leu
                     725                        730                        735
     Leu Asn Gly His Phe Val Val Ser Ala Val Glu Arg Asp Leu Val Val
                 740                        745                        750
     Lys Gly Ser Leu Leu Arg Tyr Ser Gly Thr Gly Thr Ala Val Glu Ser
             755                        760                        765
     Leu Gln Ala Ser Arg Pro Ile Leu Glu Pro Leu Thr Val Glu Val Leu
         770                        775                        780
     Ser Val Gly Lys Met Thr Pro Pro Arg Val Arg Tyr Ser Phe Tyr Leu
     785                        790                        795                        800
     Pro Lys Glu Pro Arg Glu Asp Lys Ser Ser His Pro Lys Asp Pro Arg
                     805                        810                        815
     Gly Pro Ser Val Leu His Asn Ser Val Leu Ser Leu Ser Asn Gln Val
                 820                        825                        830
     Glu Gln Pro Asp Asp Arg Pro Pro Ala Arg Trp Val Ala Gly Ser Trp
             835                        840                        845
     Gly Pro Cys Ser Ala Ser Cys Gly Ser Gly Leu Gln Lys Arg Ala Val
         850                        855                        860
     Asp Cys Arg Gly Ser Ala Gly Gln Arg Thr Val Pro Ala Cys Asp Ala
     865                        870                        875                        880
     Ala His Arg Pro Val Glu Thr Gln Ala Cys Gly Glu Pro Cys Pro Thr
                     885                        890                        895
     Trp Glu Leu Ser Ala Trp Ser Pro Cys Ser Lys Ser Cys Gly Arg Gly
                 900                        905                        910
     Phe Gln Arg Arg Ser Leu Lys Cys Val Gly His Gly Gly Arg Leu Leu
             915                        920                        925
     Ala Arg Asp Gln Cys Asn Leu His Arg Lys Pro Gln Glu Leu Asp Phe
         930                        935                        940
     Cys Val Leu Arg Pro Cys
     945                        950
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<210> 5
<211> 1104
<212> DNA
<213> homo sapiens

<400> 5
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ccagagcggg aggtagtcgt tcccatccga ctggacccgg acattaacgg ccgccgctac     120
```

```
tactggcggg gtcccgagga ctccggggat cagggactca tttttcagat cacagcattt      180
caggaggact tttacctaca cctgacgccg gatgctcagt tcttggctcc cgccttctcc      240
actgagcatc tgggcgtccc cctccagggg ctcaccgggg gctcttcaga cctgcgacgc      300
tgcttctatt ctggggacgt gaacgccgag ccggactcgt tcgctgctgt gagcctgtgc      360
ggggggctcc gcggagcctt tggctaccga ggcgccgagt atgtcattag cccgctgccc      420
aatgctagcg cgccggcggc gcagcgcaac agccagggcg cacaccttct ccagcgccgg      480
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aaccccgcca tcctacgggc cctggaccct tacaagccgc ggcgggcggg cttcggggag      600
agtcgtagcc ggcgcaggtc tgggcgcgcc aagcgtttcg tgtctatccc gcggtacgtg      660
gagacgctgg tggtcgcgga cgagtcaatg gtcaagttcc acggcgcgga cctggaacat      720
tatctgctga cgctgctggc aacggcggcg cgactctacc gccatcccag catcctcaac      780
cccatcaaca tcgttgtggt caaggtgctg cttcttagag atcgtgactc cgggcccaag      840
gtcaccggca atgcggccct gacgctgcgc aacttctgtg cctggcagaa gaagctgaac      900
aaagtgagtg acaagcaccc cgagtactgg gacactgcca tcctcttcac caggcaggac      960
ctgtgtggag ccaccacctg tgacaccctg ggcatggctg atgtgggtac catgtgtgac     1020
cccaagagaa gctgctctgt cattgaggac gatgggcttc catcagcctt caccactgcc     1080
cacgagctgg gtaaggctgg ataa                                            1104
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<210> 6
<211> 367
<212> PRT
<213> homo sapiens

<400> 6

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Met Leu Leu Leu Gly Ile Leu Thr Leu Ala Phe Ala Gly Arg Thr Ala
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Gly Gly Ser Glu Pro Glu Arg Glu Val Val Val Pro Ile Arg Leu Asp
            20                  25                  30
Pro Asp Ile Asn Gly Arg Arg Tyr Tyr Trp Arg Gly Pro Glu Asp Ser
            35                  40                  45
Gly Asp Gln Gly Leu Ile Phe Gln Ile Thr Ala Phe Gln Glu Asp Phe
    50                  55                  60
Tyr Leu His Leu Thr Pro Asp Ala Gln Phe Leu Ala Pro Ala Phe Ser
65                  70                  75                  80
Thr Glu His Leu Gly Val Pro Leu Gln Gly Leu Thr Gly Gly Ser Ser
            85                  90                  95
Asp Leu Arg Arg Cys Phe Tyr Ser Gly Asp Val Asn Ala Glu Pro Asp
            100                 105                 110
Ser Phe Ala Ala Val Ser Leu Cys Gly Gly Leu Arg Gly Ala Phe Gly
        115                 120                 125
Tyr Arg Gly Ala Glu Tyr Val Ile Ser Pro Leu Pro Asn Ala Ser Ala
    130                 135                 140
Pro Ala Ala Gln Arg Asn Ser Gln Gly Ala His Leu Leu Gln Arg Arg
145                 150                 155                 160
Gly Val Pro Gly Gly Pro Ser Gly Asp Pro Thr Ser Arg Cys Gly Val
            165                 170                 175
Ala Ser Gly Trp Asn Pro Ala Ile Leu Arg Ala Leu Asp Pro Tyr Lys
            180                 185                 190
Pro Arg Arg Ala Gly Phe Gly Glu Ser Arg Ser Arg Arg Arg Ser Gly
        195                 200                 205
Arg Ala Lys Arg Phe Val Ser Ile Pro Arg Tyr Val Glu Thr Leu Val
    210                 215                 220
Val Ala Asp Glu Ser Met Val Lys Phe His Gly Ala Asp Leu Glu His
225                 230                 235                 240
Tyr Leu Leu Thr Leu Leu Ala Thr Ala Ala Arg Leu Tyr Arg His Pro
                245                 250                 255
```

6

```
Ser Ile Leu Asn Pro Ile Asn Ile Val Val Val Lys Val Leu Leu Leu
            260                 265                 270
Arg Asp Arg Asp Ser Gly Pro Lys Val Thr Gly Asn Ala Ala Leu Thr
            275                 280                 285
Leu Arg Asn Phe Cys Ala Trp Gln Lys Lys Leu Asn Lys Val Ser Asp
            290                 295                 300
Lys His Pro Glu Tyr Trp Asp Thr Ala Ile Leu Phe Thr Arg Gln Asp
305                 310                 315                 320
Leu Cys Gly Ala Thr Thr Cys Asp Thr Leu Gly Met Ala Asp Val Gly
                325                 330                 335
Thr Met Cys Asp Pro Lys Arg Ser Cys Ser Val Ile Glu Asp Asp Gly
            340                 345                 350
Leu Pro Ser Ala Phe Thr Thr Ala His Glu Leu Gly Lys Ala Gly
            355                 360                 365
```

<210> 7
<211> 3446
<212> DNA
<213> homo sapiens

<400> 7

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gcggttccag agtgcgggct gcacggagac cgcggcagcg gccggagagc ccggcccagc    360
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tggtgcaccg ggaaggccaa gggacagatg gtgtgccaga cccgccactt ccctggggcc   1860
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aacctcaaca agcacagggt ggatggttcc tgggccaaat gggatcccta tggcccctgc   1980
tcgcgcacat gtggtggggg cgtgcagctg gccaggaggc agtgcaccaa ccccacccct   2040
gccaacgggg gcaagtactg cgagggagtg agggtgaaat accgatcctg caatctggag   2100
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